

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/729,571C
Source: 1 Fw/b
Date Processed by STIC: 10/20/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/729,571C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

3 <110> APPLICANT: Anderson et al.
 5 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)
 7 <130> FILE REFERENCE: 100966
 9 <140> CURRENT APPLICATION NUMBER: US 10/729,571C
 10 <141> CURRENT FILING DATE: 2003-12-05
 12 <150> PRIOR APPLICATION NUMBER: 60/435,272
 13 <151> PRIOR FILING DATE: 2002-12-20
 15 <150> PRIOR APPLICATION NUMBER: 60/435,167
 16 <151> PRIOR FILING DATE: 2002-12-20
 18 <150> PRIOR APPLICATION NUMBER: 60/435,087
 19 <151> PRIOR FILING DATE: 2002-12-20
 21 <150> PRIOR APPLICATION NUMBER: 60/435,527
 22 <151> PRIOR FILING DATE: 2002-12-20
 E--> 24 <160> NUMBER OF SEQ ID NOS: 76 97 (see p. 22)
 26 <170> SOFTWARE: PatentIn version 3.1

error throughout

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 768
 30 <212> TYPE: DNA
 31 <213> ORGANISM: H. pylori *insert <220>*
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(768)
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 38 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 39 1 5 10 15
 41 aaa agc ctt tta aaa gcg cga ttg ttt gat gaa atc atc tac tat ggc
 42 Lys Ser Leu Leu Lys Ala Arg Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 43 20 25 30
 45 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag
 46 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 47 35 40 45
 49 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cat gag att gaa
 50 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu
 51 50 55 60
 53 tta ttg att gtg gca tgc aac acc gcg agc gct ctg gct tta gaa gag
 54 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 55 65 70 75 80
 57 atg caa aag tat tct aaa atc cct att gtg ggc gtg att gag cca agc
 58 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser

*insert <220>
wherever <221>, <222>, or <223> is shown*

<220> is a "header" only. It never has a response.

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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61 att tta gcg atc aag cgg caa gtg gaa gat aaa aac gcc cct att tta      336
62 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu
63          100          105          110
65 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gac aac gcc      384
66 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
67          115          120          125
69 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gct act tct ctt      432
70 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
71          130          135          140
73 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
74 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
75 145          150          155          160
77 act tgc atg cat tat ttc act ccc tta gag att tta ccc gaa gtg      528
78 Thr Cys Met His Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
79          165          170          175
81 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
82 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
83          180          185          190
85 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
86 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
87          195          200          205
89 cat tcg ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
90 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
91          210          215          220
93 aaa aac aat gca tgc aca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
94 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
95 225          230          235          240
97 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
98 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
99          245          250          255
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174 <213> ORGANISM: H. pylori
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177 <222> LOCATION: (1)..(768)
179 <400> SEQUENCE: 3
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182 1          5          10          15
184 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc      96
185 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
186          20          25          30
188 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
189 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
190          35          40          45
192 caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa      192
193 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu

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OK

insert

2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

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Output Set: N:\CRF4\10202006\J729571C.raw

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194      50      55      60
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197 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
198 65      70      75      80
200 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
201 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
202      85      90      95
204 att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta      336
205 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
206      100      105      110
208 gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
209 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
210      115      120      125
212 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
213 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
214      130      135      140
216 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag      480
217 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
218 145      150      155      160
220 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
221 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
222      165      170      175
224 att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag      576
225 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
226      180      185      190
228 ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
229 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
230      195      200      205
232 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt      672
233 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
234      210      215      220
236 aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
237 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
238 225      230      235      240
240 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
241 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
242      245      250      255

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314 <210> SEQ ID NO: 5

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316 <212> TYPE: DNA

317 <213> ORGANISM: H. pylori

319 <221> NAME/KEY: CDS

320 <222> LOCATION: (1)..(768)

E--> 322 <400> SEQUENCE: 5

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323 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
324 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
325 1      5      10      15
327 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
328 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly

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insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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329      20      25      30
331 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
332 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
333      35      40      45
335 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
336 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
337      50      55      60
339 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
340 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
341 65      70      75      80
343 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
344 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
345      85      90      95
347 att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta      336
348 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
349      100      105      110
351 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aat gcc      384
352 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
353      115      120      125
355 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
356 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
357      130      135      140
359 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
360 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
361 145      150      155      160
363 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc gaa gtg      528
364 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
365      165      170      175
367 att att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
368 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
369      180      185      190
371 ggc tat ttt atg gag cat ttt gcc ctt tca aca ccc ccc cta ctc atc      624
372 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
373      195      200      205
375 cat tcg ggc gat gct att gta gga tat ttg cag caa aaa tac gcc ctt      672
376 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
377      210      215      220
379 aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
380 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
381 225      230      235      240
383 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
384 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
385      245      250      255
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458 <211> LENGTH: 749
459 <212> TYPE: DNA
460 <213> ORGANISM: H. pylori
462 <221> NAME/KEY: CDS
463 <222> LOCATION: (1)..(747)

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insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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467	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
468	1			5						10			15				
470	aaa	agc	ctt	tta	aaa	gcg	caa	ttg	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
471	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
472				20						25				30			
474	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
475	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
476				35						40				45			
478	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	aaa	192
479	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys	
480		50					55				60						
482	tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gaa	gag	240
483	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
484	65				70					75				80			
486	atg	caa	aag	cat	tcc	aaa	atc	cct	att	gtg	ggc	gtg	att	gag	cca	agc	288
487	Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
488				85						90				95			
490	att	tta	gcg	atc	aag	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336
491	Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
492				100						105				110			
494	gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tcc	aac	gct	tat	gac	aac	gcc	384
495	Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
496				115						120				125			
498	ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tcg	cat	tta	gcc	act	tct	ctt	432
499	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
500		130					135					140					
502	ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	ggg	ggc	gaa	ttg	tta	gaa	480
503	Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Gly	Glu	Leu	Leu	Glu	
504	145					150					155				160		
506	act	tgc	atg	cgt	tat	tat	ttc	act	ccc	tta	aag	att	tta	cct	gaa	gtg	528
507	Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val	
508				165						170				175			
510	att	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576
511	Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
512				180						185				190			
514	ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624
515	Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
516				195						200				205			
518	cat	tcg	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
519	His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
520			210				215						220				
522	aag	aaa	aat	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720
523	Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
524	225					230					235				240		
526	gat	gtg	atc	tgg	cta	gaa	aaa	cag	gct	aa							749
527	Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala								
528					245												

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

600 <210> SEQ ID NO: 9
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 602 <212> TYPE: DNA
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 606 <222> LOCATION: (1)..(768)

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611	1 5 10 15	
613	aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc	96
614	Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
615	20 25 30	
617	gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
618	Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
619	35 40 45	
621	caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga	192
622	Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly	
623	50 55 60	
625	tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
626	Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
627	65 70 75 80	
629	atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc	288
630	Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
631	85 90 95	
633	att tta gcg atc aag caa caa gta aaa gat aaa aac gcc tct att ttg	336
634	Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu	
635	100 105 110	
637	gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc	384
638	Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
639	115 120 125	
641	ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
642	Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
643	130 135 140	
645	ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa	480
646	Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
647	145 150 155 160	
649	act tgc atg cgt tat tat ttc act ccg tta gag atc ttg cct gaa gtg	528
650	Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val	
651	165 170 175	
653	gtt att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag	576
654	Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
655	180 185 190	
657	ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc	624
658	Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile	
659	195 200 205	
661	cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt	672
662	His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Lys Tyr Ala Leu	
663	210 215 220	

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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665 aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc      720
666 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
667 225                230                235                240
669 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
670 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
671                245                250                255
743 <210> SEQ ID NO: 11
744 <211> LENGTH: 749
745 <212> TYPE: DNA
746 <213> ORGANISM: H. pylori
748 <221> NAME/KEY: CDS
749 <222> LOCATION: (1)..(747)
E--> 751 <400> SEQUENCE: 11
752 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
753 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
754 1                5                10                15
756 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
757 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
758                20                25                30
760 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
761 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
762                35                40                45
764 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
765 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
766                50                55                60
768 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
769 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
770 65                70                75                80
772 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
773 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
774                85                90                95
776 att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta      336
777 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
778                100               105               110
780 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
781 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
782                115               120               125
784 cta aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt      432
785 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
786                130               135               140
788 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag      480
789 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
790 145               150               155               160
792 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
793 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
794                165               170               175
796 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
797 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
798                180               185               190

```

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

800 ggc tat ttt atg gag cat ttt gcc ctt cca acc ccc ccc cta ctc atc      624
801 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
802      195      200      205
804 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac acc ctt      672
805 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
806      210      215      220
808 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc      720
809 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
810 225      230      235      240
812 gat gtg gtt tgg cta gaa aaa cag gct aa      749
813 Asp Val Val Trp Leu Glu Lys Gln Ala
814      245
886 <210> SEQ ID NO: 13
887 <211> LENGTH: 768
888 <212> TYPE: DNA
889 <213> ORGANISM: H. pylori
891 <221> NAME/KEY: CDS
892 <222> LOCATION: (1)..(768)
E--> 894 <400> SEQUENCE: 13
895 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
896 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
897 1      5      10      15
899 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
900 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
901      20      25      30
903 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
904 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
905      35      40      45
907 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
908 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
909      50      55      60
911 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
912 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
913 65      70      75      80
915 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
916 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
917      85      90      95
919 att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta      336
920 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
921      100      105      110
923 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gcc      384
924 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
925      115      120      125
927 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
928 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
929      130      135      140
931 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
932 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
933 145      150      155      160

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insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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935 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
936 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
937          165          170          175
939 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
940 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
941          180          185          190
943 ggc tat ttt atg gag cat ttt gcc ctt tta acg ccc ccc cta ctc atc      624
944 Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile
945          195          200          205
947 cat tct ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
948 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
949          210          215          220
951 aag aaa aat gca cac tca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
952 Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly
953 225          230          235          240
955 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
956 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
957          245          250          255
1029 <210> SEQ ID NO: 15
1030 <211> LENGTH: 768
1031 <212> TYPE: DNA
1032 <213> ORGANISM: H. pylori
1034 <221> NAME/KEY: CDS
1035 <222> LOCATION: (1)..(768)
E--> 1037 <400> SEQUENCE: 15
1038 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1039 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1040 1          5          10          15
1042 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
1043 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
1044          20          25          30
1046 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1047 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1048          35          40          45
1050 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
1051 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
1052          50          55          60
1054 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1055 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1056 65          70          75          80
1058 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc      288
1059 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1060          85          90          95
1062 att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta      336
1063 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1064          100          105          110
1066 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gac aac gcc      384
1067 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1068          115          120          125

```

Insert <220>

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1070 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
1071 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1072      130                      135                      140
1074 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa      480
1075 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1076 145                      150                      155                      160
1078 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc aaa gta      528
1079 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val
1080                      165                      170                      175
1082 atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag      576
1083 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
1084                      180                      185                      190
1086 ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
1087 Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Leu Leu Ile
1088      195                      200                      205
1090 cat tcg ggc gat gct att gtg gga tat ttg caa caa aaa tac gcc ctt      672
1091 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
1092      210                      215                      220
1094 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1095 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1096 225                      230                      235                      240
1098 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1099 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1100      245                      250                      255
1172 <210> SEQ ID NO: 17
1173 <211> LENGTH: 768
1174 <212> TYPE: DNA
1175 <213> ORGANISM: H. pylori
1177 <221> NAME/KEY: CDS
1178 <222> LOCATION: (1)..(768)
E--> 1180 <400> SEQUENCE: 17
1181 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1182 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1183 1                      5                      10                      15
1185 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1186 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1187      20                      25                      30
1189 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1190 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1191      35                      40                      45
1193 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1194 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1195      50                      55                      60
1197 tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag      240
1198 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1199 65                      70                      75                      80
1201 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1202 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1203      85                      90                      95

```

insert (2207)

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1205 att tta gcg atc aaa caa cag gta aaa gat aaa aac gcc ccc att tta      336
1206 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1207           100                      105                      110
1209 gtg cta ggc aca aaa gcg acg att caa tct aac gct tac gat aac gct      384
1210 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1211           115                      120                      125
1213 ctg aaa cga caa ggc tat ttg aac gtt tcg cat tta gcc act tcc ctt      432
1214 Leu Lys Arg Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1215           130                      135                      140
1217 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1218 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1219 145           150                      155                      160
1221 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
1222 Thr Cys Met Arg Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
1223           165                      170                      175
1225 atc att tta ggt tgt acg cat ttt ccc ttg atc gct caa aaa att gag      576
1226 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1227           180                      185                      190
1229 ggc tat ttt atg gaa cat ttt gcc ttt cca acg ccc ccc cta ctc atc      624
1230 Gly Tyr Phe Met Glu His Phe Ala Phe Pro Thr Pro Pro Leu Leu Ile
1231           195                      200                      205
1233 cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1234 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1235           210                      215                      220
1237 aag aaa aat gca cac gca tta cct aaa gtg gaa ttt cat gcg agc ggc      720
1238 Lys Lys Asn Ala His Ala Leu Pro Lys Val Glu Phe His Ala Ser Gly
1239 225           230                      235                      240
1241 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1242 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1243           245                      250                      255

```

1315 <210> SEQ ID NO: 19

1316 <211> LENGTH: 768

1317 <212> TYPE: DNA

1318 <213> ORGANISM: H. pylori

1320 <221> NAME/KEY: CDS

1321 <222> LOCATION: (1)..(768)

E--> 1323 <400> SEQUENCE: 19

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1324 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1325 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1326 1           5           10           15
1328 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1329 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1330           20           25           30
1332 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1333 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1334           35           40           45
1336 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1337 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1338           50           55           60

```

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

1340 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1341 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1342 65              70              75              80
1344 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1345 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1346              85              90              95
1348 att tta gcg atc aaa caa caa gta aag gat aaa aac gcc ccc att tta      336
1349 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1350              100              105              110
1352 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gct      384
1353 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1354              115              120              125
1356 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt      432
1357 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1358              130              135              140
1360 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa      480
1361 Phe Val Pro Leu Ile Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
1362 145              150              155              160
1364 act tgc atg cgt tat tat ttc act ccc tta gag att tta cct gaa gtg      528
1365 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
1366              165              170              175
1368 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
1369 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1370              180              185              190
1372 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc ata ctc atc      624
1373 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
1374              195              200              205
1376 cat tct ggc gac gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
1377 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1378              210              215              220
1380 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1381 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1382 225              230              235              240
1384 gat atg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1385 Asp Met Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1386              245              250              255

```

1458 <210> SEQ ID NO: 21

1459 <211> LENGTH: 768

1460 <212> TYPE: DNA

1461 <213> ORGANISM: H. pylori

1463 <221> NAME/KEY: CDS

1464 <222> LOCATION: (1)..(768)

E--> 1466 <400> SEQUENCE: 21

```

1467 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1468 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1469 1              5              10              15
1471 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1472 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1473              20              25              30

```

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

1475 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1476 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1477          35                      40                      45
1479 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1480 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1481          50                      55                      60
1483 tta ttg att gta gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1484 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1485 65                      70                      75                      80
1487 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1488 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1489          85                      90                      95
1491 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
1492 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1493          100                     105                     110
1495 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
1496 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1497          115                     120                     125
1499 ctg aaa caa caa ggc tat ttg aat gtt tgc cat tta gcc act tct ctt      432
1500 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1501          130                     135                     140
1503 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1504 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1505 145                     150                     155                     160
1507 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
1508 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
1509          165                     170                     175
1511 att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
1512 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1513          180                     185                     190
1515 agc tat ttt atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
1516 Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
1517          195                     200                     205
1519 cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1520 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1521          210                     215                     220
1523 aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1524 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1525 225                     230                     235                     240
1527 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1528 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1529          245                     250                     255

```

1601 <210> SEQ ID NO: 23

1602 <211> LENGTH: 768

1603 <212> TYPE: DNA

1604 <213> ORGANISM: H. pylori

1607 <221> NAME/KEY: CDS

1608 <222> LOCATION: (1)..(768)

E--> 1610 <400> SEQUENCE: 23

insert (2207)

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

1611	atg	aaa	ata	ggc	gtt	ttt	gat	agc	ggg	gtg	gga	ggg	ttt	agc	gtt	tta	48
1612	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1613	1			5					10				15				
1615	aaa	agc	ctt	tta	aaa	gcg	caa	cta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
1616	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
1617			20					25					30				
1619	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
1620	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
1621			35					40				45					
1623	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	gga	192
1624	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
1625		50				55					60						
1627	tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	ctg	gct	tta	gaa	gag	240
1628	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
1629	65				70				75			80					
1631	atg	caa	aaa	tat	tcc	aaa	atc	cct	att	gtg	ggc	gtg	att	gag	cca	agc	288
1632	Met	Gln	Lys	Tyr	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
1633			85					90				95					
1635	att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	ccc	att	tta	336
1636	Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
1637			100					105				110					
1639	gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tct	aac	gct	tat	gat	aac	gcc	384
1640	Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
1641			115					120				125					
1643	ctg	aaa	caa	caa	ggc	tat	ttg	aac	att	tcg	cat	tta	gcc	act	tct	ctt	432
1644	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu	
1645		130				135					140						
1647	ttt	gtg	ccc	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
1648	Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
1649	145				150				155			160					
1651	act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528
1652	Thr	Cys	Met	Arg	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
1653			165					170				175					
1655	atc	att	tta	ggg	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576
1656	Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
1657			180					185				190					
1659	agc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	tta	ctc	atc	624
1660	Ser	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
1661			195					200				205					
1663	cat	tct	ggc	gat	gct	att	gtg	gaa	tac	ttg	caa	caa	aaa	tac	gcc	ctt	672
1664	His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
1665		210				215					220						
1667	aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720
1668	Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
1669	225				230				235			240					
1671	gat	gtg	atc	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768
1672	Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu		
1673			245					250				255					
1745	<210> SEQ ID NO: 25																

RAW SEQUENCE LISTING

DATE: 10/20/2006

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TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

1746 <211> LENGTH: 768
 1747 <212> TYPE: DNA
 1748 <213> ORGANISM: H. pylori
 1750 <221> NAME/KEY: CDS
 1751 <222> LOCATION: (1)..(768)

insert <2207

E--> 1753 <400> SEQUENCE: 25

1754	atg	aaa	ata	ggc	ggt	ttt	gat	agc	ggg	gtg	gga	ggg	ttt	agc	ggt	tta	48
1755	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1756	1			5					10				15				
1758	aaa	agc	ctt	tta	aaa	gcg	caa	tta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
1759	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
1760			20					25					30				
1762	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
1763	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
1764			35				40				45						
1766	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	aaa	att	gaa	192
1767	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu	
1768		50				55			60								
1770	tta	tta	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	ctg	gct	tta	gaa	gag	240
1771	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
1772	65				70				75				80				
1774	atg	caa	aag	cat	tcc	aaa	atc	ccc	att	gtg	ggc	gtg	att	gag	cca	agc	288
1775	Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
1776				85				90					95				
1778	att	tta	gcg	atc	aaa	caa	caa	gtg	aaa	gat	aaa	aac	acc	cct	att	tta	336
1779	Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Thr	Pro	Ile	Leu	
1780			100					105					110				
1782	gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tct	aac	gct	tac	gat	aac	gcc	384
1783	Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
1784			115					120					125				
1786	ctg	aaa	caa	caa	ggc	tat	ttg	aag	gtt	tcg	cat	ttg	gcc	act	tct	ctt	432
1787	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Lys	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
1788		130				135			140								
1790	ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
1791	Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
1792	145				150				155				160				
1794	act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gaa	atc	tta	cct	gaa	gtg	528
1795	Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
1796			165					170					175				
1798	ggt	att	tta	ggc	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576
1799	Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
1800			180					185					190				
1802	ggc	tat	ttt	atg	gaa	cat	ttt	gcc	ctt	cca	acg	ccc	ccc	cta	ctc	atc	624
1803	Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile	
1804			195					200					205				
1806	cat	tct	ggc	gac	gct	att	gtg	gga	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
1807	His	Ser	Gly	Asp	Ala	Ile	Val	Gly	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
1808		210					215						220				
1810	aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/729,571C

DATE: 10/20/2006

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Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

1811 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 1812 225 230 235 240
 1814 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
 1815 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 1816 245 250 255
 1888 <210> SEQ ID NO: 27
 1889 <211> LENGTH: 768
 1890 <212> TYPE: DNA
 1891 <213> ORGANISM: H. pylori
 1893 <221> NAME/KEY: CDS
 1894 <222> LOCATION: (1)..(768) *insert <2207*

E--> 1896 <400> SEQUENCE: 27

1897 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta 48
 1898 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1899 1 5 10 15
 1901 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96
 1902 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
 1903 20 25 30
 1905 gat agc gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 1906 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 1907 35 40 45
 1909 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa 192
 1910 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
 1911 50 55 60
 1913 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gaa 240
 1914 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 1915 65 70 75 80
 1917 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc 288
 1918 Met. Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 1919 85 90 95
 1921 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta 336
 1922 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 1923 100 105 110
 1925 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc 384
 1926 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 1927 115 120 125
 1929 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
 1930 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 1931 130 135 140
 1933 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa 480
 1934 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 1935 145 150 155 160
 1937 act tgc atg cgt tat tat ttc act cca tta gag atc ttg cct gaa gtg 528
 1938 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 1939 165 170 175
 1941 gtt att tta ggc tgc acg cat ttt ccc ttg atc gct cac caa att gag 576
 1942 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
 1943 180 185 190
 1945 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1946 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
1947      195      200      205
1949 cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1950 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1951      210      215      220
1953 aag aaa aac gca tgt gca ttc cct aaa gta gaa ttt cat gcg agc ggc      720
1954 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1955 225      230      235      240
1957 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1958 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1959      245      250      255
2031 <210> SEQ ID NO: 29
2032 <211> LENGTH: 768
2033 <212> TYPE: DNA
2034 <213> ORGANISM: H. pylori
2036 <221> NAME/KEY: CDS
2037 <222> LOCATION: (1)..(768)
E--> 2039 <400> SEQUENCE: 29
2040 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2041 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2042 1      5      10      15
2044 aaa agc ctt tta aaa gtg caa tta ttt gat gaa atc atc tat tat ggc      96
2045 Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
2046      20      25      30
2048 gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2049 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2050      35      40      45
2052 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa      192
2053 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
2054 50      55      60
2056 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gga gag      240
2057 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu
2058 65      70      75      80
2060 atg caa aag tat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
2061 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
2062      85      90      95
2064 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
2065 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2066      100      105      110
2068 gta cta ggg aca aaa gcg acg att cga tcc aac gct tat gac aac gcc      384
2069 Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala
2070      115      120      125
2072 ctg aaa caa caa ggc tat ttg aat att tcg cat tta gcc act tct ctt      432
2073 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
2074      130      135      140
2076 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
2077 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
2078 145      150      155      160
2080 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528

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RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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2081 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2082                165                170                175
2084 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag      576
2085 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
2086                180                185                190
2088 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
2089 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2090                195                200                205
2092 cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac gcc ctt      672
2093 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
2094                210                215                220
2096 aag aaa aac gca tgc gca ttc cct aaa gta gaa ttc cat gcg agc ggc      720
2097 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2098 225                230                235                240
2100 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
2101 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2102                245                250                255
2174 <210> SEQ ID NO: 31
2175 <211> LENGTH: 768
2176 <212> TYPE: DNA
2177 <213> ORGANISM: H. pylori
2179 <221> NAME/KEY: CDS
2180 <222> LOCATION: (1)..(768)
E--> 2182 <400> SEQUENCE: 31
2183 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2184 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2185 1                5                10                15
2187 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
2188 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
2189                20                25                30
2191 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2192 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2193                35                40                45
2195 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
2196 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
2197                50                55                60
2199 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
2200 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
2201 65                70                75                80
2203 atg caa aag cat tcc aaa atc cct att gtg ggt gtg att gag cca agc      288
2204 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
2205                85                90                95
2207 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
2208 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2209                100               105               110
2211 gtg tta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
2212 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
2213                115               120               125
2215 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt      432

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insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

2216	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
2217		130					135					140					
2219	ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
2220	Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
2221	145					150					155				160		
2223	act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528
2224	Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
2225					165					170				175			
2227	ggt	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	cac	caa	att	gag	576
2228	Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu	
2229			180					185					190				
2231	ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	tta	ctc	atc	624
2232	Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
2233		195					200						205				
2235	cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aaa	tac	acc	ctt	672
2236	His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Thr	Leu	
2237		210				215					220						
2239	aag	aaa	aat	gca	tgc	gcg	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720
2240	Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
2241	225				230					235				240			
2243	gat	gtg	ggt	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768
2244	Asp	Val	Val	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu		
2245			245					250					255				

2317 <210> SEQ ID NO: 33

2318 <211> LENGTH: 765

2319 <212> TYPE: DNA

2320 <213> ORGANISM: H. pylori

2322 <221> NAME/KEY: CDS

2323 <222> LOCATION: (1)..(765)

E--> 2325 <400> SEQUENCE: 33

2326	atg	aaa	ata	ggc	ggt	ttt	gat	agc	ggt	gtg	gga	ggg	ttt	agc	ggt	tta	48
2327	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
2328	1			5					10					15			
2330	aaa	agc	ctt	tta	aaa	gcg	caa	cta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
2331	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
2332			20					25					30				
2334	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
2335	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
2336		35					40					45					
2338	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	aaa	192
2339	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys	
2340		50				55					60						
2342	tta	ttg	att	gtg	gca	tgc	aac	acc	gca	agc	gct	ctg	gct	tta	gaa	gag	240
2343	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
2344	65				70					75				80			
2346	atg	caa	aag	cat	tcc	aaa	atc	cct	ggt	gtg	ggc	gtg	att	gag	cca	agc	288
2347	Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Val	Val	Gly	Val	Ile	Glu	Pro	Ser	
2348				85				90					95				
2350	att	tta	gcg	atc	aaa	cgg	caa	gtg	aaa	gat	aaa	aac	gcc	cct	att	ttg	336

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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2351 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2352           100                      105                      110
2354 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gat aac gcc      384
2355 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
2356           115                      120                      125
2358 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
2359 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
2360           130                      135                      140
2362 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa      480
2363 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
2364 145                      150                      155                      160
2366 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
2367 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2368           165                      170                      175
2370 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
2371 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
2372           180                      185                      190
2374 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
2375 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2376           195                      200                      205
2378 cat tct ggc gat gct att gtg gaa tat ttg caa caa aat tac gcc ctt      672
2379 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu
2380           210                      215                      220
2382 aag aaa aac gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
2383 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2384 225                      230                      235                      240
2386 gat gtg gtt tgg cta gaa aaa caa gct aaa gaa tgg ctt aaa ttg      765
2387 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2388           245                      250                      255
3614 <210> SEQ ID NO: 75
3615 <211> LENGTH: 19
3616 <212> TYPE: DNA
3617 <213> ORGANISM: primer
3619 <400> SEQUENCE: 75
E--> 3620 tfatgcaaca aatggacga

```

19

invalid response - see item 10 on Error Summary Sheet

invalid nucleotide designator

same error in sequence 76

VERIFICATION SUMMARY

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:58

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

L:36 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:179 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:322 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:465 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:608 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
L:751 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:894 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:1037 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:1180 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:1323 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:19
L:1466 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21
L:1610 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23
L:1753 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:1896 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27
L:2039 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:2182 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:2325 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:33
L:3620 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:24 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (76) Counted (97)

10/729,571C

22

<210> 97 last sequence in submitted file
<211> 32
<212> PRT
<213> Enterococcus faecium

<400> 97

Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
1 5 10 15

Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu Ile Asp
20 25 30